

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(I) APPLICANT: Vreeland, Valerie, Ng, Kwan

(ii) TITLE OF INVENTION: Recombinant Vanadium Haloperoxidases
And Their Uses

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew LLP

(B) STREET: Two Embarcadero Center, Eighth Floor

(C) CITY: San Francisco

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Not yet assigned

(B) FILING DATE: 08-AUG-1998

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:

(B) REGISTRATION NUMBER:

(C) REFERENCE/DOCKET NUMBER: 023070-087100US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 576-0200

(B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2931 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 228..2258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCGGACAAG CCTTGGAAGA GAGGTTGCC AATTCAACAG AGCGAGGCC GTGAAGGTGT 60

5 GGAGGACACG TGCTACAAGC TGATCCACGA GAGCCTCAAC TTCCCTACTG ATACGGGAGT 120

TTGTACTGCG CCGCGTTGCC AAAAACCGCA ACTTTAAACA GCGCTCGCGA GCGCCACATG 180

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[illegible]

TTT GCC ATC GAC ATA TCC GGT CCC GCA TTC TCG GCT ACG ACA ATA CCC 956
Phe Ala Ile Asp Ile Ser Gly Pro Ala Phe Ser Ala Thr Thr Ile Pro
230 235 240

CCG GTA CCT ACC CTT TCC TCT CCT GAG CTC GCC GCT CAG TTG GCG GAG 1004
Pro Val Pro Thr Leu Ser Ser Pro Glu Leu Ala Ala Gln Leu Ala Glu
245 250 255

CTA TAC TGG ATG GCG CTG GCC AGG GAT GTA CCC TTT ATG CAG TAT GGC 1052
Leu Tyr Trp Met Ala Leu Ala Arg Asp Val Pro Phe Met Gln Tyr Gly
260 265 270 275

ACC GAC GAA ATT ACC ACT ACC GCG GCA GCC AAC CTC GCT GGA ATG GGA 1100
Thr Asp Glu Ile Thr Thr Thr Ala Ala Ala Asn Leu Ala Gly Met Gly
280 285 290

GGC TTC CCA AAT CTG GAC GCC GTG TCG ATA GGG TCC GAT GGT ACG GTG 1148
Gly Phe Pro Asn Leu Asp Ala Val Ser Ile Gly Ser Asp Gly Thr Val
295 300 305

GAC CCG TTC TCC CAG CTC TTC CGA GCG ACC TTC GTT GGT GTT GAA ACG 1196
Asp Pro Phe Ser Gln Leu Phe Arg Ala Thr Phe Val Gly Val Glu Thr
310 315 320

GGG CCC TTT GTC TCT CAG CTG CTC GTG AAC AGC TTC ACC ATC GAC GCT 1244
Gly Pro Phe Val Ser Gln Leu Leu Val Asn Ser Phe Thr Ile Asp Ala
325 330 335

ATT ACG GTC GAA CCG AAG CAG GAG ACA TTC GCC CCC GAC TTG AAC TAT 1292
Ile Thr Val Glu Pro Lys Gln Glu Thr Phe Ala Pro Asp Leu Asn Tyr
340 345 350 355

ATG GTC GAT TTT GAC GAA TGG CTG AAC ATT CAG AAT GGT GGA CCC CCG 1340
Met Val Asp Phe Asp Glu Trp Leu Asn Ile Gln Asn Gly Gly Pro Pro
360 365 370

GCC GGC CCC GAA GAG TTA GAC GAA GAG CTG CGT TTT ATC CGT AAC GCC 1388
Ala Gly Pro Glu Glu Leu Asp Glu Glu Leu Arg Phe Ile Arg Asn Ala
375 380 385

CGC	GAC	CTG	GCC	AGG	GTC	TCC	TTC	GTG	GAC	AAT	ATC	AAC	ACC	GAA	GCT	1436
Arg	Asp	Leu	Ala	Arg	Val	Ser	Phe	Val	Asp	Asn	Ile	Asn	Thr	Glu	Ala	
		390					395					400				

TAT CGC GGG TCT CTT ATC CTA CTT GAG CTG GGA GCC TTC AGC AGG CCC 1484
Tyr Arg Gly Ser Leu Ile Leu Leu Glu Leu Gly Ala Phe Ser Arg Pro
405 410 415

GGT ATC AAC GGT CCA TTC ATC GAC AGT GAT CGG CAG GCG GGC TTC GTC 1532
Gly Ile Asn Gly Pro Phe Ile Asp Ser Asp Arg Gln Ala Gly Phe Val
420 425 430 435

AAC TTC GGC ACG TCT CAC TAC TTC AGA TTG ATA GGT GCC GCC GAG CTG 1580
Asn Phe Gly Thr Ser His Tyr Phe Arg Leu Ile Gly Ala Ala Glu Leu

	440										445					450					
5	GCG	CAG	CGT	GCC	TCG	TGT	TAC	CAA	AAG	TGG	CAG	GTG	CAT	CGA	TTT	GCA	1628				
	Ala	Gln	Arg	Ala	Ser	Cys	Tyr	Gln	Lys	Trp	Gln	Val	His	Arg	Phe	Ala					
				455					460					465							
10	CGC	CCC	GAG	GCT	CTC	GGG	GGT	ACC	CTC	CAC	AAC	ACC	ATC	GCG	GGG	GAT	1676				
	Arg	Pro	Glu	Ala	Leu	Gly	Gly	Thr	Leu	His	Asn	Thr	Ile	Ala	Gly	Asp					
			470					475					480								
15	CTA	GAT	GCA	GAC	TTC	GAC	ATC	TCC	CTT	CTT	GAA	AAT	GAT	GAG	CTC	TTG	1724				
	Leu	Asp	Ala	Asp	Phe	Asp	Ile	Ser	Leu	Leu	Glu	Asn	Asp	Glu	Leu	Leu					
		485					490					495									
20	AAA	CGT	GTG	GCG	GAG	ATA	AAT	GCG	GCG	CAG	AAT	CCC	AAC	AAC	GAG	GTC	1772				
	Lys	Arg	Val	Ala	Glu	Ile	Asn	Ala	Ala	Gln	Asn	Pro	Asn	Asn	Glu	Val					
	500					505					510				515						
25	ACC	TAC	CTT	CTT	CCA	CAA	GCT	ATC	CAA	GTG	GGA	TCG	CCA	ACG	CAC	CCT	1820				
	Thr	Tyr	Leu	Leu	Pro	Gln	Ala	Ile	Gln	Val	Gly	Ser	Pro	Thr	His	Pro					
					520					525					530						
30	TCC	TAC	CCG	TCC	GGC	CAC	GCT	ACC	CAA	AAT	GGA	GCA	TTT	GCC	ACA	GTT	1868				
	Ser	Tyr	Pro	Ser	Gly	His	Ala	Thr	Gln	Asn	Gly	Ala	Phe	Ala	Thr	Val					
				535					540					545							
35	CTG	AAG	GCC	CTC	ATT	GGC	CTA	GAT	CGG	GGA	GGT	GAG	TGC	TTC	CCT	AAC	1916				
	Leu	Lys	Ala	Leu	Ile	Gly	Leu	Asp	Arg	Gly	Gly	Glu	Cys	Phe	Pro	Asn					
			550				555						560								
40	CCC	GTG	TTC	CCA	AGC	GAT	GAC	GGC	CTG	GAA	CTA	ATC	AAC	TTC	GAA	GGG	1964				
	Pro	Val	Phe	Pro	Ser	Asp	Asp	Gly	Leu	Glu	Leu	Ile	Asn	Phe	Glu	Gly					
		565					570					575									
45	GCA	TGC	CTT	ACA	TAT	GAG	GGA	GAG	ATC	AAC	AAG	CTC	GCG	GTC	AAC	GTC	2012				
	Ala	Cys	Leu	Thr	Tyr	Glu	Gly	Glu	Ile	Asn	Lys	Leu	Ala	Val	Asn	Val					
	580					585					590					595					
50	GCA	TTT	GGG	AGG	CAG	ATG	CTG	GGC	ATC	CAC	TAT	CGG	TTC	GAC	GGT	ATC	2060				
	Ala	Phe	Gly	Arg	Gln	Met	Leu	Gly	Ile	His	Tyr	Arg	Phe	Asp	Gly	Ile					
				600						605					610						
55	CAA	GGC	CTA	CTT	CTC	GGA	GAG	ACA	ATC	ACT	GTA	CGA	ACA	CTT	CAC	CAG	2108				
	Gln	Gly	Leu	Leu	Leu	Gly	Glu	Thr	Ile	Thr	Val	Arg	Thr	Leu	His	Gln					
				615				620						625							
60	GAG	CTG	ATG	ACG	TTC	GCC	GAG	GAA	GCC	ACC	TTT	GAA	TTC	CGC	TTA	TTC	2156				
	Glu	Leu	Met	Thr	Phe	Ala	Glu	Glu	Ala	Thr	Phe	Glu	Phe	Arg	Leu	Phe					
			630</																		

GCT TAGTGCAGAA AATAATAATT GTCGGATGCT TAAAATGCAC CCACGACCAA 2305
Ala

5 GTCGTCGAGT CACGTCGCCG GAGCATCCTT CAGCGAAAAA GGAGAGTAAC CTATATGCTA 2365
TAGAGGAGAA CCACGGAGTA CAATGCAGGT TCTTTTACCA TGTACATTGG ATTGCAGTAA 2425
GTGCGGTTAG AGAGGGATAC GTTAAACGTG CTTGCCTGTG TATATGATAC ATTTGTCATG 2485
10 GAAATATTAG AATGCGTTGA CTTGACTTCA CCATGAAATA CCATGATCGC GTGGTGTGCT 2545
GCTTTCACCT GTCGGAGCGG TACGTAAGAT GTGCTTTCTA CTGAGCCGTT TGTGTTTAGT 2605
15 CCATTCCGCG TGGCAGTGTA AACAAAGAGG ATGTAGTCTC GCCCTCAGTT TGGAGAGTAC 2665
CGTAGGTGGC AGGACGTATA TCTCTGGTAG CGGTCTGTGA AGAACTTCCA CAAGACCGTT 2725
TACGTTTGGT TGTTTAGTCG ATGCCTCTTC GTTACTTGAC CGATCCATTG AGAGTACCTG 2785
20 TACCAGTATG GTGTAAGACA TATTTTTCTC CTGTTATGGA TCTGTAGAAC AGCTAGGTGT 2845
TGTTTTATAC ACAGGATGCT ATAAAATAGG GATGTTGATA ATGGCATCGG TACTCATGAA 2905
25 ACCGCAAAAT GGCATAGAT ATTCCC 2931

0040-2305-2931

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Cys His Ala Ala Asp Thr Thr Arg Gly Ser Pro Met Pro Asp
 1 5 10 15

Thr Gly Val Leu Arg Leu Leu Thr Ser Glu Gln Arg Ala Lys Gly Trp
 20 25 30

Arg Arg Gln Leu Glu Gly Glu Lys Ser Leu Gly Phe His Pro Ser Glu
 35 40 45

Thr Pro Tyr Ile Lys Tyr Leu Glu Gly Ser Glu Thr Trp Lys Lys Val
 50 55 60

Lys Leu Pro Thr Asp Gly Ile Ser Ala Ser Lys Ile Leu Gly Lys Ile
 65 70 75 80

Met Ala Arg Val Arg Ile Ala Thr Ala Leu Ala Val Val Leu Ala Ala
 85 90 95

Pro Cys Leu Ala Phe Asp Glu Val Thr Ala Ser Gly Val Phe Pro Glu
 100 105 110

Glu His Lys His Thr Gly Glu Gly Arg His Leu Gln Thr Cys Thr Asn
 115 120 125

Ser Asp Asp Ala Leu Asp Pro Thr Ala Pro Asn Arg Arg Asp Asn Val
 130 135 140

Ala Phe Ala Ser Arg Arg Asp Ala Ala Arg Arg Glu Arg Asp Gly Thr
 145 150 155 160

Gly Thr Val Cys Gln Ile Thr Asn Gly Glu Thr Asp Leu Ala Thr Met
 165 170 175

Phe His Lys Ser Leu Pro His Asp Glu Leu Gly Gln Val Thr Ala Asp
 180 185 190

Asp Phe Ala Ile Leu Glu Asp Cys Ile Leu Asn Gly Asp Phe Ser Ile
 195 200 205

Cys Glu Asp Val Pro Ala Gly Asp Pro Ala Gly Arg Leu Val Asn Pro
 210 215 220

Thr Ala Ala Phe Ala Ile Asp Ile Ser Gly Pro Ala Phe Ser Ala Thr
 225 230 235 240

Thr Ile Pro Pro Val Pro Thr Leu Ser Ser Pro Glu Leu Ala Ala Gln

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Thr His Pro Ser Tyr Pro Ser Gly His Ala Thr Gln Asn Gly Ala Phe
530 535 540

Ala Thr Val Leu Lys Ala Leu Ile Gly Leu Asp Arg Gly Gly Glu Cys

	545		550		555		560									
	Phe	Pro	Asn	Pro	Val	Phe	Pro	Ser	Asp	Asp	Gly	Leu	Glu	Leu	Ile	Asn
					565					570						575
5	Phe	Glu	Gly	Ala	Cys	Leu	Thr	Tyr	Glu	Gly	Glu	Ile	Asn	Lys	Leu	Ala
				580					585					590		
	Val	Asn	Val	Ala	Phe	Gly	Arg	Gln	Met	Leu	Gly	Ile	His	Tyr	Arg	Phe
10			595					600					605			
	Asp	Gly	Ile	Gln	Gly	Leu	Leu	Leu	Gly	Glu	Thr	Ile	Thr	Val	Arg	Thr
	610						615					620				
15	Leu	His	Gln	Glu	Leu	Met	Thr	Phe	Ala	Glu	Glu	Ala	Thr	Phe	Glu	Phe
	625					630					635					640
	Arg	Leu	Phe	Thr	Gly	Glu	Val	Ile	Lys	Leu	Phe	Gln	Asp	Gly	Thr	Phe
					645					650					655	
20	Ser	Ile	Asp	Gly	Asp	Met	Cys	Ser	Gly	Leu	Val	Tyr	Thr	Gly	Val	Ala
			660						665					670		
25	Asp	Cys	Gln	Ala												
			675													